

SEQUENCE LISTING

<110> Wyeth

Ling, Vincent

Carreno, Beatriz M.

<120> USE OF B7-H3 AS AN IMMUNOREGULATORY AGENT

<130> 08702.6108-00000

<160> 35

<170> PatentIn version 3.1

<210> 1

<211> 951

<212> DNA

<213> Homo sapiens

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<211> 316

<212> PRT

<213> Homo sapiens

<400> 2

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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu

35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn

50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala

65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe

85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val

100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp

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120

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Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys

130

135

140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr

145

150

155

160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val

165

170

175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr

180

185

190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu

195

200

205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn

210

215

220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln
225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser
245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln
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Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys His
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Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala
305 310 315

<210> 3

<211> 951

<212> DNA

<213> Mouse

<400> 3

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<210> 4

<211> 316

<212> PRT

<213> Mouse

<400> 4

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Val Ser Glu Asp Pro Val Val Ala Leu Val Asp Thr Asp Ala Thr Leu

35 40 45

Arg Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn

50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr

65 70 75 80

Glu Gly Arg Asp Gln Gly Ser Ala Tyr Ser Asn Arg Thr Ala Leu Phe

85 90 95

Pro Asp Leu Leu Val Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val

100 105 110

Arg Val Thr Asp Glu Gly Ser Tyr Thr Cys Phe Val Ser Ile Gln Asp

115 120 125

Phe Asp Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys

130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asn Met

145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val

165 170 175

Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr

180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu

195

200

205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn

210

215

220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln

225

230

235

240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser

245

250

255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg

260

265

270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln

275

280

285

Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro

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Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala

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310

315

<210> 5

<211> 1605

<212> DNA

<213> Homo sapiens

<400> 5

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<210> 6

<211> 534

<212> PRT

<213> Homo sapiens

<400> 6

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Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln

20 25 30

Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu

35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn

50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala
 65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe
 85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val
 100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp
 115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys
 130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr
 145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val
 165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr

180

185

190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu

195

200

205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn

210

215

220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln

225

230

235

240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val

245

250

255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro

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265

270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr

275

280

285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly
290 295 300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln
305 310 315 320

Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
355 360 365

Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser
370 375 380

Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln
385 390 395 400

Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu

405

410

415

Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala

420

425

430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp

435

440

445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro

450

455

460

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu

465

470

475

480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys

485

490

495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly

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505

510

Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp

515

520

525

Asp Gly Gln Glu Ile Ala

530

<210> 7

<211> 112

<212> PRT

<213> Homo sapience

<400> 7

Ala Leu Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly

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Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser

20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu

35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn

50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu

65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe

85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala

100 105 110

<210> 8

<211> 112

<212> PRT

<213> Homo sapiens

<220>

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<222> (53)..(53)

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<220>

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<223> Q, or R, or any other amino acid

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<221> MISC_FEATURE

<222> (2)..(2)

<223> L, or V, or any other amino acid

<220>

<221> MISC_FEATURE

<222> (22)..(22)

<223> C, or R, or any other amino acid

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Thr Asp Ala Thr Leu Xaa Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser

20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu

35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn

50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu
 65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe
 85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala
 100 105 110

<210> 9

<211> 1670

<212> DNA

<213> Chimera

<400> 9

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accgatgcca ccctgtgctg ctcctttctcc cctgagcctg gcttcagcct ggcacagctc 180

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<210> 10

<211> 482

<212> PRT

<213> Chimera

<400> 10

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5

10

15

Leu Leu Phe Pro Ser Met Ala Ser Met Leu Glu Val Gln Val Pro Glu

20

25

30

Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser

35

40

45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp

50

55

60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln

65

70

75

80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu

85

90

95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala

100

105

110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser

115

120

125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met

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Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile			
145	150	155	160
Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln			
	165	170	175
Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met			
	180	185	190
Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val			
195	200	205	
Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu			
210	215	220	
Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr			
225	230	235	240
Phe Pro Pro Glu Ala Gly Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile			
	245	250	255

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly

260

265

270

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile

275

280

285

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp

290

295

300

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His

305

310

315

320

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg

325

330

335

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys

340

345

350

Ala Phe Ala Cys Ala Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu

355

360

365

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr

370

375

380

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu

385

390

395

400

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp

405

410

415

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val

420

425

430

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu

435

440

445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His

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Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro

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480

Gly Lys

<210> 11

<211> 2324

<212> DNA

<213> Chimera

<400> 11

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aatgcccag gtaagtcact agaccagagc tccactcccc ggagaatggt aagtgtctata	1500
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ggactggatg agtggcaagg ctttcgcatg cgccgtcaac acaaagacc tcccagcgcc	1860
catcgagaga accatctcaa aacccaaagg tgagagctgc agcctgactg catgggggct	1920
gggatgggca taaggataaa ggtctgtgtg gacagccttc tgcttcagcc atgacctttg	1980
tgtatgtttc taccctcaca gggtcagtaa gagctccaca ggtatatgtc ttgcctccac	2040
cagaagaaga gatgactaag aaacaggtea ctctgacctg catgggcaca gacttcatgc	2100
ctgaagacat ttacgtggag tggaccaaca acgggaaaac agagctaaac tacaagaaca	2160
ctgaaccagt cctggactct gatgggttctt acttcatgta cagcaagctg agagtggaaa	2220
agaagaactg ggtggaaaga aatagctact cctgttcagt ggtccacgag ggtctgcaca	2280
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<210> 12

<211> 700

<212> PRT

<213> Chimera

<400> 12

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala

1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Leu Glu Val Gln Val Pro Glu

20 25 30

Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser

35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp

50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln

65 70 75 80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu

85

90

95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala

100

105

110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser

115

120

125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met

130

135

140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile

145

150

155

160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln

165

170

175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met

180

185

190

Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu Arg Val Val

195	200	205
Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu		
210	215	220
Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln Arg Ser Pro		
225	230	235
		240
Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu		
	245	250
		255
Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro Glu Pro Gly		
260	265	270
Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys		
275	280	285
Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly Ser Ala Tyr		
290	295	300
Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala		
305	310	315
		320

Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr

325

330

335

Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln

340

345

350

Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu Pro Asn Lys

355

360

365

Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser Ser Tyr Arg

370

375

380

Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln Gly Val Pro

385

390

395

400

Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu Gln Gly Leu

405

410

415

Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala Asn Gly Thr

420

425

430

Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Gly

435

440

445

Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Gly

450

455

460

Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys

465

470

475

480

Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe

485

490

495

Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val

500

505

510

Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile

515

520

525

Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr

530

535

540

His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
 545 550 555 560

Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val
 565 570 575

Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro
 580 585 590

Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu
 595 600 605

Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp
 610 615 620

Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr
 625 630 635 640

Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser
 645 650 655

Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu

660

665

670

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His

675

680

685

His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys

690

695

700

<210> 13

<211> 1670

<212> DNA

<213> Mouse

<400> 13

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acggatgcca ccctacgctg ctctttttcc ccagagcctg gcttcagtct ggcacagctc 180

aacctcatct ggcagctgac agacacaaaa cagctgggtgc acagcttcac ggagggccgg 240

gaccaaggca gtgcctactc caaccgcaca gcgctcttcc ctgacctgtt ggtgcaaggc 300

aatgcgtcct tgaggctgca gcgcgtccga gtaaccgacg agggcagcta cacctgcttt 360

gtgagcattc aggactttga cagcgctgct gttagcctgc aggtggccgc cccctactcg	420
aagcccagca tgaccctgga gcccaacaag gacctacgtc caggggaacat ggtgaccatc	480
acgtgctcta gctaccaggg ctatccggag gccgaggtgt tctggaagga tggacagggga	540
gtgcccttga ctggcaatgt gaccacatcc cagatggcca acgagcgggg cttgttcgat	600
gttcacagcg tgctgagggg ggtgctgggt gctaacggca cctacagctg cctgggtacgc	660
aacccggtgt tgcagcaaga tgctcacggc tcagtcacca tcacagggca gccctgaca	720
ttccccctg aggcagggtc ggggtccgag ccccgccgac cgacaatcaa gccctgtcct	780
ccatgcaa at gcccaggtaa gtcactagac cagagctcca ctcccgagg aatggtaagt	840
gctataaaca tccctgcact agaggataag ccatgtacag atccatttcc atctctctc	900
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tgtactcatg atctccctga gcccatagt cacatgtgtg gtgggtggatg tgagcgagga	1020
tgaccagat gtccagatca gctgggttgt gaacaacgtg gaagtacaca cagctcagac	1080
acaaacccat agagaggatt acaacagtac tctccgggtg gtcagtgcc tccccatcca	1140
gcaccaggac tggatgagtg gcaaggcttt cgcattgcgc gtcaacaaca aagacctccc	1200
agcgcccatc gagagaacca tctcaaaacc caaagggtgag agctgcagcc tgactgcatg	1260

ggggctggga tgggcataag gataaaggtc tgtgtggaca gccttctgct tcagccatga 1320

cctttgtgta tgtttctacc ctcacagggt cagtaagagc tccacaggta tatgtcttgc 1380

ctccaccaga agaagagatg actaagaaac aggtcactct gacctgcatg gtcacagact 1440

tcatgcctga agacatttac gtggagtgga ccaacaacgg gaaaacagag ctaaactaca 1500

agaacactga accagtcctg gactctgatg gttcttactt catgtacagc aagctgagag 1560

tggaaaagaa gaactgggtg gaaagaaata gctactcctg ttcagtgggc cacgaggggc 1620

tgcacaatca ccacacgact aagagcttct cccggactcc gggtaaata 1670

<210> 14

<211> 482

<212> PRT

<213> Mouse

<400> 14

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala

1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Val Glu Val Gln Val Ser Glu

20 25 30

Asp Pro Val Val Ala Leu Val Asp Thr Asp Ala Thr Leu Arg Cys Ser

35

40

45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp

50

55

60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg

65

70

75

80

Asp Gln Gly Ser Ala Tyr Ser Asn Arg Thr Ala Leu Phe Pro Asp Leu

85

90

95

Leu Val Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Thr

100

105

110

Asp Glu Gly Ser Tyr Thr Cys Phe Val Ser Ile Gln Asp Phe Asp Ser

115

120

125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met

130

135

140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asn Met Val Thr Ile
 145 150 155 160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Lys
 165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
 180 185 190

Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val
 195 200 205

Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu
 210 215 220

Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Leu Thr
 225 230 235 240

Phe Pro Pro Glu Ala Gly Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile
 245 250 255

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly

260

265

270

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile

275

280

285

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp

290

295

300

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His

305

310

315

320

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg

325

330

335

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys

340

345

350

Ala Phe Ala Cys Ala Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu

355

360

365

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr

370

375

380

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu

385

390

395

400

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp

405

410

415

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val

420

425

430

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu

435

440

445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His

450

455

460

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro

465

470

475

480

Gly Lys

<210> 15

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<220>

<221> Misc_feature

<222> (1)..(3)

<223> ALA, or another amino acid sequence

<220>

<221> Misc_feature

<222> (26)..(27)

<223> SP, or another amino acid sequence

<220>

<221> Misc_feature

<222> (52)..(62)

<223> FAEGQDQGSAY, or another amino acid sequence

<220>

<221> Misc_feature

<222> (67)..(79)

<223> ALFPDLLAQGNAS, or another amino acid sequence

<220>

<221> Misc_feature

<222> (86)..(102)

<223> RVADEGSFTCFVSIRDF, or another amino acid sequence

<220>

<221> Misc_feature

<222> (107)..(107)

<223> V, or another amino acid sequence

<220>

<221> Misc_feature

<222> (7)..(17)

<223> PEDPVVALVGT, or another amino acid sequence

<400> 15

Xaa Xaa Xaa Val Gln Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1

5

10

15

Xaa Asp Ala Thr Leu Cys Cys Ser Phe Xaa Xaa Glu Pro Gly Phe Ser

20

25

30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu

35

40

45

Val His Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala Asn

50

55

60

Arg Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu

65

70

75

80

Arg Leu Gln Arg Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

85

90

95

Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Ala Ala Xaa Ser Leu Gln Val Ala

100

105

110

<210> 16

<211> 3

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 16

Val Gln Val

1

<210> 17

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 17

Asp Ala Thr Leu Cys Cys Ser Phe

1

5

<210> 18

<211> 24

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 18

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr

1 5 10 15

Asp Thr Lys Gln Leu Val His Ser

20

<210> 19

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 19

Ala Asn Arg Thr

1

<210> 20

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 20

Leu Arg Leu Gln Arg Val

1 5

<210> 21

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 21

Gly Ser Ala Ala

1

<210> 22

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved among mammals

<400> 22

Ser Leu Gln Val Ala

1 5

<210> 23

<211> 112

<212> PRT

<213> Artificial sequence

<220>

<223> Conserved amino acids in human B7-H3 V1 and V2

<220>

<221> Misc_feature

<222> (2)..(2)

<223> L or V, or another amino acid

<220>

<221> Misc_feature

<222> (22)..(22)

<223> C or R, or another amino acid

<220>

<221> Misc_feature

<222> (53)..(53)

<223> A or T, or another amino acid

<220>

<221> Misc_feature

<222> (56)..(56)

<223> Q or R, or another amino acid

<400> 23

Ala Xaa Glu Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly

1 5 10 15

Thr Asp Ala Thr Leu Xaa Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser

20 25 30

Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu

35 40 45

Val His Ser Phe Xaa Glu Gly Xaa Asp Gln Gly Ser Ala Tyr Ala Asn

50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu

65 70 75 80

Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe

85 90 95

Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala

100 105 110

<210> 24

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 24

ggggacaagt ttgtacaaaa aagcaggctc caccatgctg cgtcggcgagg gcagc 55

<210> 25

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 25

ggggaccact ttgtacaaga aagctggggt caggctatattt cttgtccatc 50

<210> 26

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 26

ctctggggggg aatgtcatag gc 22

<210> 27

<211> 55

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 27

ggggacaagt ttgtacaaaa aagcaggctc caccatgctt cgaggatggg gtggc 55

<210> 28

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 28

ggggaccact ttgtacaaga aagctggggt caagcaattt cttgtccgctc 50

<210> 29

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 29

agcttttgctg agggccagga c 21

<210> 30

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 30

ctgggagcac tgtggttctg cc

22

<210> 31

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 31

ctggcacagc tcaacctcat c

21

<210> 32

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 32

accaggcagc tgtaggtgcc

20

<210> 33

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 33

ctgtgatggt gactgagccg tg

22

<210> 34

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 34

cgcggtgcgtg tggcggatga g

21

<210> 35

<211> 22

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 35

tacaggaatc agcactgggt tc

22